



Putative trait-based retention of oral-derived microbes along the oral–gut axis in bamboo-eating pandas

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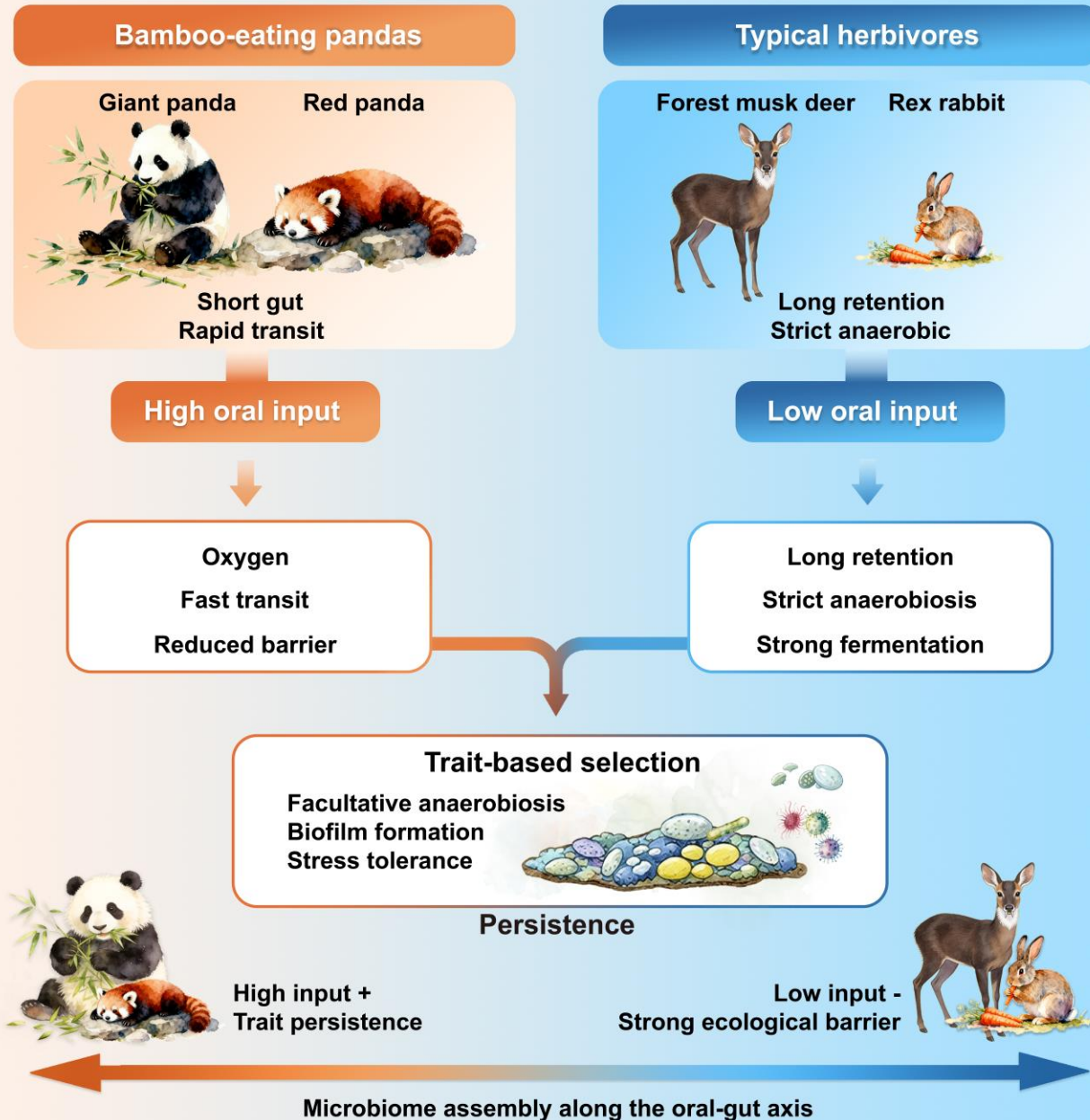


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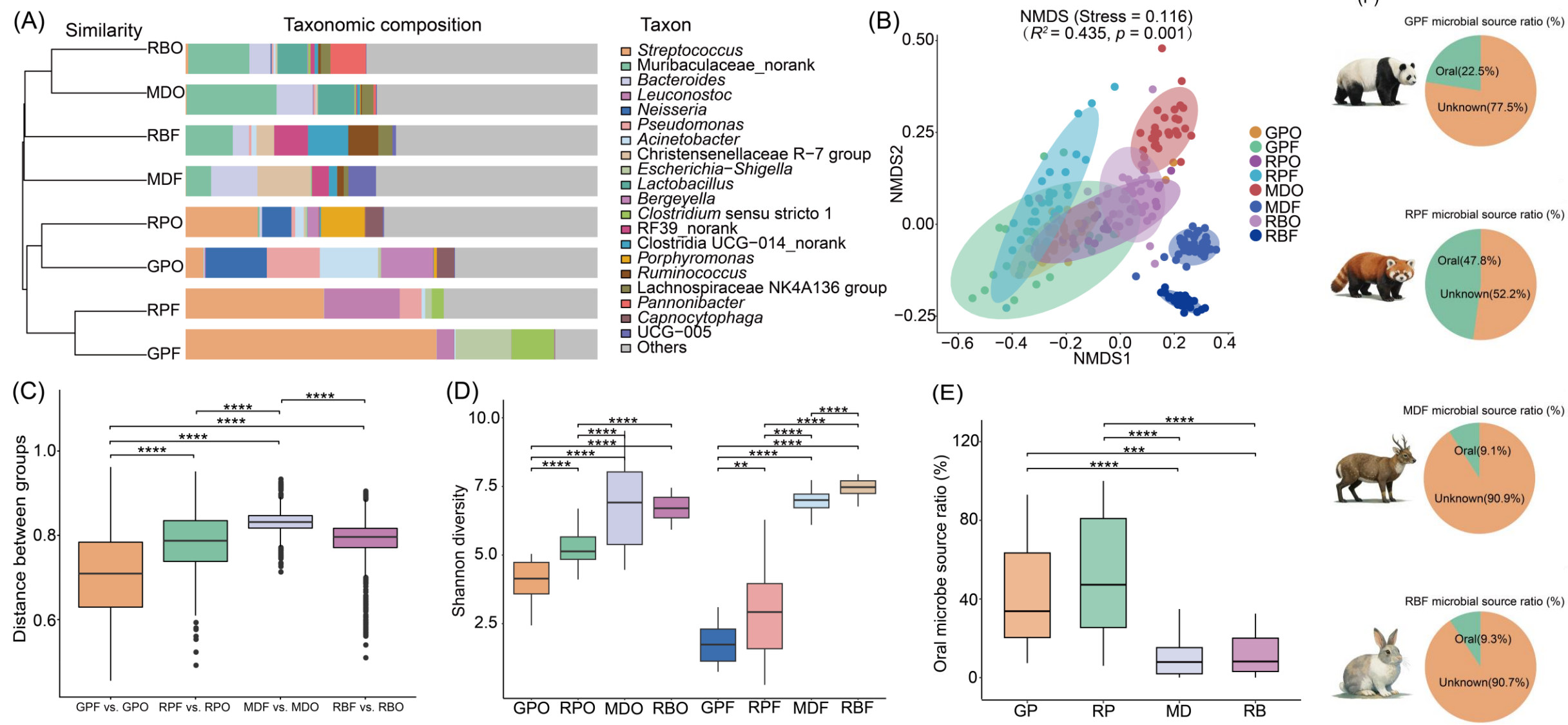
Introduction and Highlights



- Bamboo-eating pandas show stronger oral–gut microbial connectivity.
- The estimated oral-source contributions to the gut microbiota of giant pandas and red pandas are 22.5% and 47.8%, respectively.
- Retained taxa show enrichment of putative adaptive traits, including facultative anaerobiosis, biofilm formation, and stress tolerance.
- Higher oral microbial input and putative trait-based filtering may jointly promote selective retention.



Bamboo-eating pandas show relatively higher oral–gut microbial connectivity



Oral-derived microbes in bamboo-eating pandas are concentrated in a few dominant taxa

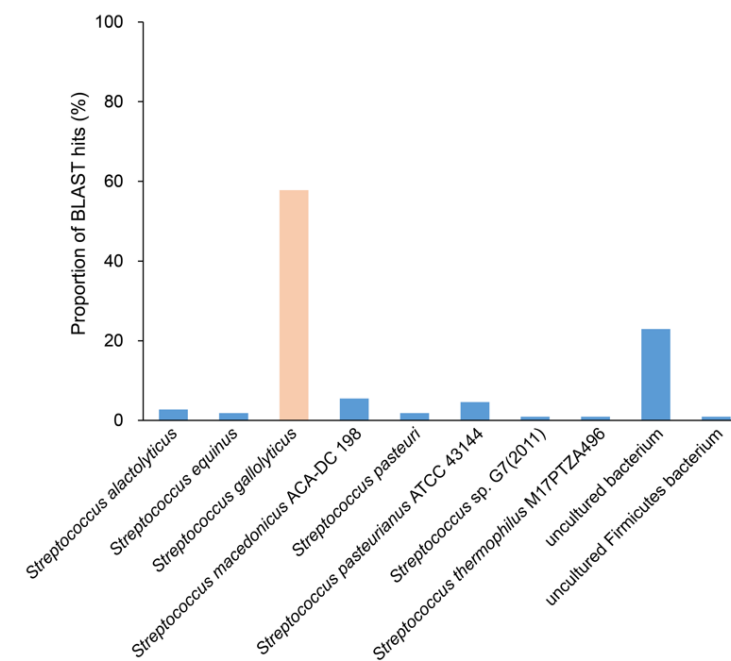
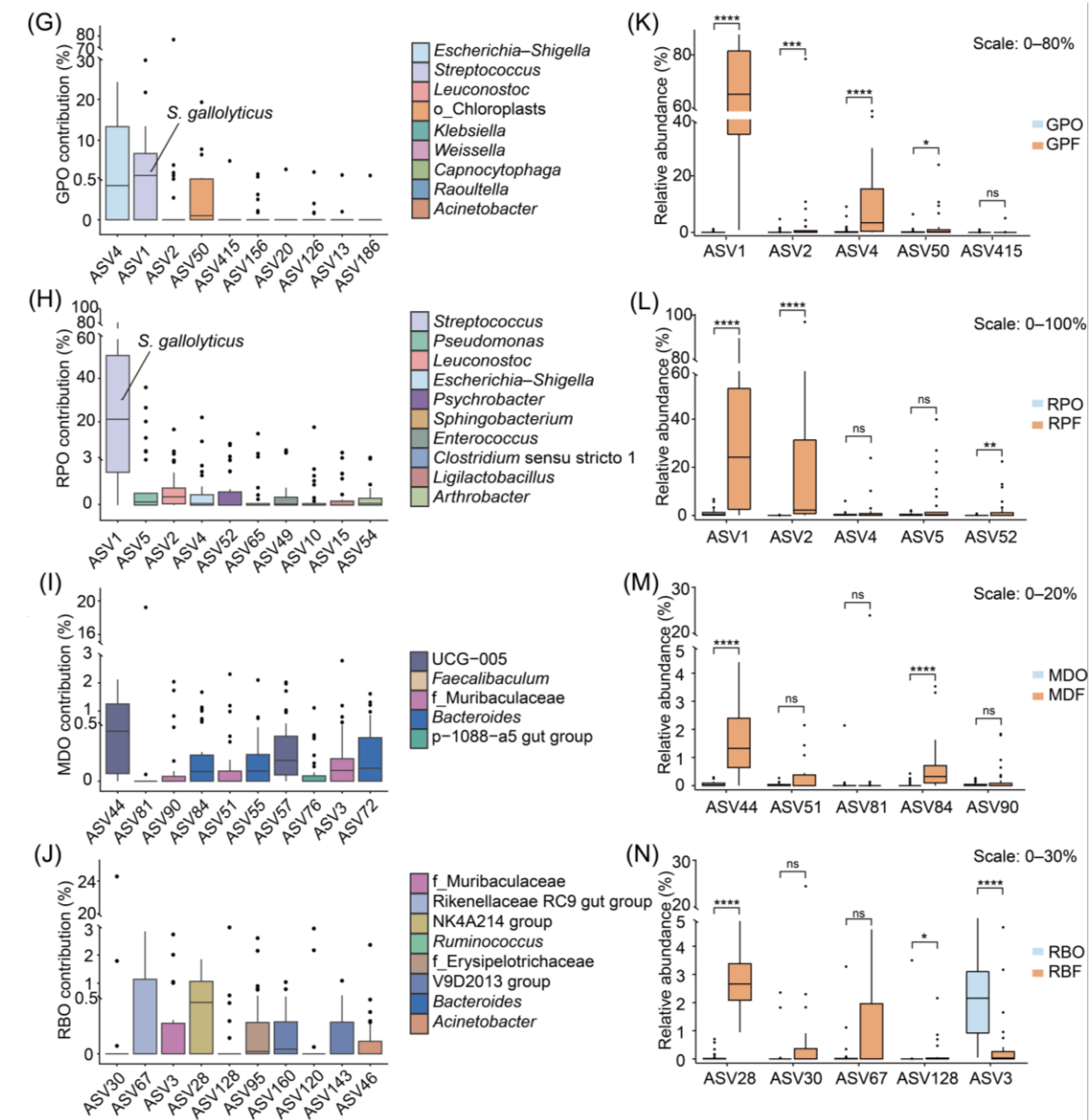


Figure S9. BLAST species-level annotation results for ASV1

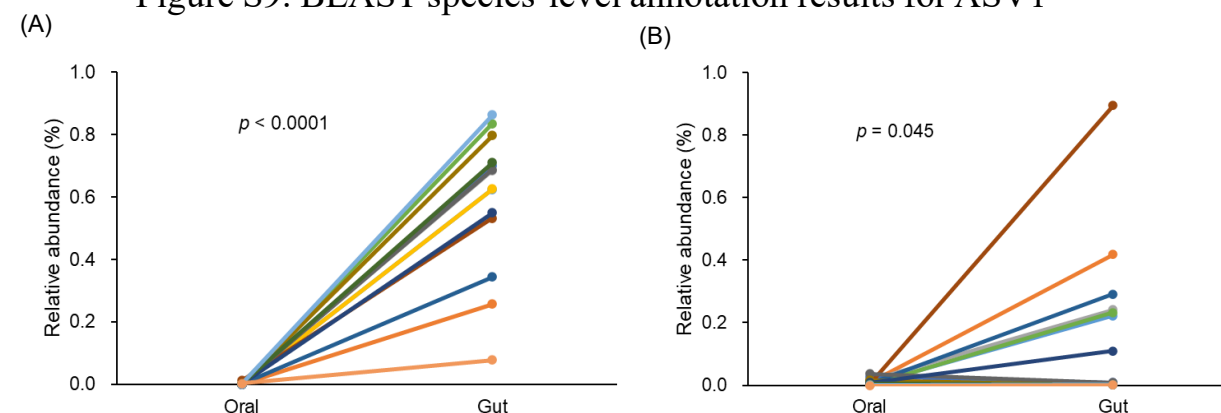
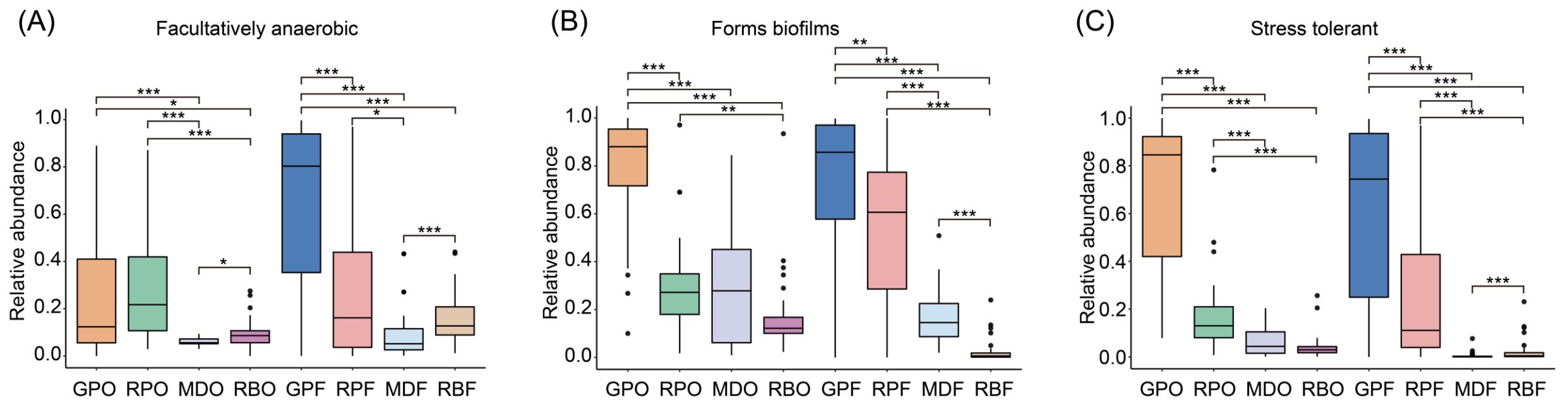


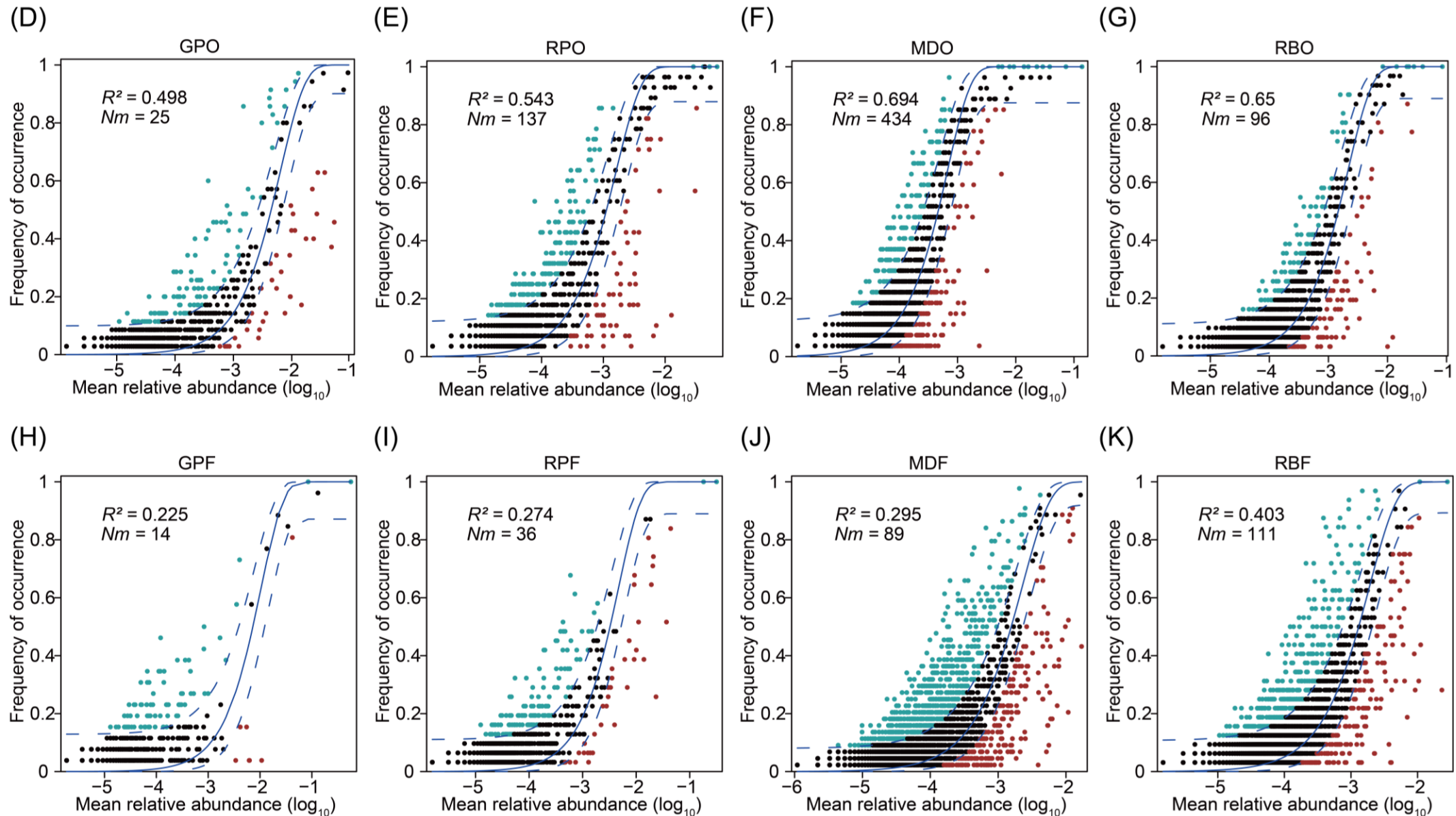
Figure S10. Changes in the relative abundance of ASV1 in paired oral-gut samples from giant pandas (A) and red pandas (B).



Retained oral-derived taxa in pandas are enriched in adaptive ecological traits



Gut microbiota assembly in bamboo-eating pandas deviates more from neutral expectations





Summary

- ❑ Oral-derived microbes may undergo selective retention rather than simply entering and accumulating in the gut;
- ❑ Putative adaptive traits may facilitate the persistence of certain taxa in the panda gut;
- ❑ Microbial input and host filtering may jointly contribute to gut microbiota assembly in pandas.

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